

SEQUENCE LISTING

<110> FEDER, J.N.
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<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY4,
EXPRESSED HIGHLY IN PROSTATE, COLON, AND LUNG

<130> D0039NP/3053-4117US3

<140> TBA

<141> 2001-09-26

<150> 60/235,833

<151> 2000-09-27

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<150> 60/305,351

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<151> 2001-08-17

<160> 60

<170> PatentIn Ver. 2.1

<210> 1

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<213> Homo sapiens

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gctgtgctag gtaacttgac aatcatctac attgtgcgga ctgagcacag cctgcatgag 180
cccattgtata tatttctttg catgctttca ggcattgaca tcctcatctc cacctcatcc 240
atgccccaaa tgctggccat cttctggttc aattccacta ccatccagtt tgatgcttgt 300
ctgctacaga tgtttgccat ccactcctta tctggcatgg aatccacagt gctgctggcc 360
atggcttttg accgctatgt ggccatctgt caccactgc gccatgccac agtacttacg 420
ttgcctcgtg tcaccaaatt tggtgtggct gctgtggtgc ggggggctgc actgatggca 480

ccccttcttg tcttcatcaa gcagctgccc ttctgccgct ccaatatcct ttcccattcc 540
 tactgcctac accaagatgt catgaagctg gcctgtgatg atatccgggt caatgtcgtc 600
 tatggcctta tegtcatcat ctccgccatt ggccctggact cacttctcat ctcccttctca 660
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 ggcacttgcg tctctcatgt gtgtgctgtg ttcatatctt atgtaccttt cattggattg 780
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<210> 2

<211> 318

<212> PRT

<213> Homo sapiens

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 20 25 30

Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile
 35 40 45

Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile
 50 55 60

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser
 65 70 75 80

Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln
 85 90 95

Phe Asp Ala Cys Leu Leu Gln Met Phe Ala Ile His Ser Leu Ser Gly
 100 105 110

Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala
 115 120 125

Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val
 130 135 140

Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala
 145 150 155 160

Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile
 165 170 175

Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys
 180 185 190

Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser
 195 200 205

Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile
 210 215 220

Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe
 225 230 235 240

Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro
 245 250 255

Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser
 260 265 270

Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val
 275 280 285

Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg
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Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
 305 310 315

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 atctgaggcc tggttttctg gaaagagacc agagactgac cttattgcat gtcatacaac 240
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 ccacaccctc agttagtttt gtataatctt aggcttgatg agaataaat cttagtcttg 360
 aaggcttttaa aggggaagaa atagctgtct gtgttagtgg tgtgtcagtc agcaggagaa 420
 cctgctaggg gtggaaggag gagggtagga gtatagccta gaccatgagt agataccccg 480
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 cacaaaaact tggaaaacac aagttcatag actgggcaac cctgagtagt ggagagatca 1320
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<211> 2034

<212> DNA

<213> Homo sapiens

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 caaatatgaa actggttggg gaatctccat tttttcaata ttattttctt ctttgttttc 180
 ttgtacata taattattaa taccctgact aggttgtggt tggagggtta ttacttttca 240
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 agaatggtac atctagagaa catttgccaa aggcctaagc acggcaaagg aaaataaaca 360
 cagaatataa taaaatgaga taatctagct taaaactata acttcctctt cagaactccc 420
 aaccacattg gatctcagaa aaatactgtc ttcaaaatga cttctacaga gaagaaataa 480
 tttttcctct ggacactagc acttaagggg aagattggaa gtaaagcctt gaaaagagta 540
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 cctgtttttc ctatttaatt ttcttatcaa ccctttaatt aggcaaagat attattagta 660
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 gcctagaaca taatagtgtt tatgcttgac accggttatt tttcatcaaa cctgattcct 1680
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 gttacacaga gtaaatacacc agaagcctgg atttctgaaa aaactgtgca gagccaaacc 1920
 tctgtcattt gcaactccca cttgtatttg tacgaggcag ttggataagt gaaaaataaa 1980
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<211> 80

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
 oligos

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 tatggaagga atgtgtgacc 80

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic
 oligos

<400> 6

actgagcaca gcctgcatga 20

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

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 oligos

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<210> 8

<211> 311
 <212> PRT
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<400> 8

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			20					25					30		
Tyr	Phe	Ser	Ile	Ile	Val	Gly	Asn	Gly	Thr	Leu	Leu	Phe	Ile	Ile	Trp
		35					40					45			
Ser	Asp	His	Ser	Leu	His	Glu	Pro	Met	Tyr	Tyr	Phe	Leu	Ala	Val	Leu
	50					55					60				
Ala	Ser	Met	Asp	Leu	Gly	Met	Thr	Leu	Thr	Thr	Met	Pro	Thr	Val	Leu
65					70					75					80
Gly	Val	Leu	Val	Leu	Asn	Gln	Arg	Glu	Ile	Val	His	Gly	Ala	Cys	Phe
				85					90					95	
Ile	Gln	Ser	Tyr	Phe	Ile	His	Ser	Leu	Ala	Ile	Val	Glu	Ser	Gly	Val
			100					105						110	
Leu	Leu	Ala	Met	Ser	Tyr	Asp	Arg	Phe	Val	Ala	Ile	Cys	Thr	Pro	Leu
		115					120					125			
His	Tyr	Asn	Ser	Ile	Leu	Thr	Asn	Ser	Arg	Val	Met	Lys	Met	Ala	Leu
		130				135					140				
Gly	Ala	Leu	Leu	Arg	Gly	Phe	Val	Ser	Ile	Val	Pro	Pro	Ile	Met	Pro
145				150					155					160	
Leu	Phe	Trp	Phe	Pro	Tyr	Cys	His	Ser	His	Val	Leu	Ser	His	Ala	Phe
				165					170					175	
Cys	Leu	His	Gln	Asp	Val	Met	Lys	Leu	Ala	Cys	Ala	Asp	Ile	Thr	Phe
		180						185					190		
Asn	Leu	Ile	Tyr	Pro	Val	Val	Leu	Val	Ala	Leu	Thr	Phe	Phe	Leu	Asp
		195					200					205			
Ala	Leu	Ile	Ile	Ile	Phe	Ser	Tyr	Val	Leu	Ile	Leu	Lys	Lys	Val	Met
		210				215					220				
Gly	Ile	Ala	Ser	Gly	Glu	Glu	Arg	Lys	Lys	Ser	Leu	Asn	Thr	Cys	Val

09966459 092604

225 230 235 240
 Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
 245 250 255
 Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
 260 265 270
 Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
 275 280 285
 Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Ile Leu Arg Leu
 290 295 300
 Leu Ser Lys His Ser Arg Thr
 305 310

 <210> 9
 <211> 307
 <212> PRT
 <213> MOUSE

 <400> 9
 Met Trp Ser Asn Ile Ser Ala Ala Pro Phe Leu Leu Thr Gly Phe Pro
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 Gly Leu Glu Ala Ala His His Trp Ile Ser Ile Pro Phe Phe Ala Ile
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 Tyr Ile Ser Val Leu Leu Gly Asn Gly Thr Leu Leu Tyr Leu Ile Lys
 35 40 45
 Asp Asp His Asn Leu His Glu Pro Met Tyr Tyr Phe Leu Ala Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Thr Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Ala Val Leu Trp Val Asn His Arg Glu Ile Arg His Gly Ala Cys Phe
 85 90 95
 Leu Gln Ala Tyr Ile Ile His Ser Leu Ser Ile Val Glu Ser Gly Val
 100 105 110
 Leu Leu Ala Met Ser Tyr Asp Arg Phe Val Ala Ile Cys Thr Pro Leu
 115 120 125

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His Tyr Asn Ser Ile Leu Thr Asn Ser Arg Val Ile Ala Ile Gly Leu
130 135 140

Gly Val Val Leu Arg Gly Phe Leu Ser Leu Val Pro Pro Ile Leu Pro
145 150 155 160

Leu Phe Trp Phe Ser Tyr Cys Arg Ser His Val Leu Ser His Ala Phe
165 170 175

Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Ala Asp Ile Thr Phe
180 185 190

Asn Arg Ile Tyr Pro Val Val Leu Val Ala Leu Thr Phe Phe Leu Asp
195 200 205

Ala Leu Ile Ile Val Phe Ser Tyr Val Leu Ile Leu Lys Thr Val Met
210 215 220

Gly Ile Ala Ser Gly Glu Glu Arg Ala Lys Ala Leu Asn Thr Cys Val
225 230 235 240

Ser His Ile Ser Cys Val Leu Val Phe Tyr Ile Thr Val Ile Gly Leu
245 250 255

Thr Phe Ile His Arg Phe Gly Lys Asn Ala Pro His Val Val His Ile
260 265 270

Thr Met Ser Tyr Val Tyr Phe Leu Phe Pro Pro Phe Met Asn Pro Ile
275 280 285

Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Arg Ser Val Leu His Leu
290 295 300

Leu Ser Val
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<212> PRT
<213> HUMAN

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20 25 30

Tyr Val Cys Ile Leu Leu Gly Asn Gly Met Leu Leu Tyr Leu Ile Lys
 35 40 45
 His Asp His Ser Leu His Glu Pro Met Tyr Tyr Phe Leu Thr Met Leu
 50 55 60
 Ala Gly Thr Asp Leu Met Val Thr Leu Thr Thr Met Pro Thr Val Met
 65 70 75 80
 Gly Ile Leu Trp Val Asn His Arg Glu Ile Ser Ser Val Gly Cys Phe
 85 90 95
 Leu Gln Ala Tyr Phe Ile His Ser Leu Ser Val Val Glu Ser Gly Ser
 100 105 110
 Leu Leu Ala Met Ala Tyr Asp Arg Phe Ile Ala Ile Arg Asn Pro Leu
 115 120 125
 Arg Tyr Ala Ser Ile Phe Thr Asn Thr Arg Val Ile Ala Leu Gly Val
 130 135 140
 Gly Val Phe Leu Arg Gly Phe Val Ser Ile Leu Pro Val Ile Leu Arg
 145 150 155 160
 Leu Phe Ser Phe Ser Tyr Cys Lys Ser His Val Ile Thr Arg Ala Phe
 165 170 175
 Cys Leu His Gln Glu Ile Met Arg Leu Ala Cys Ala Asp Ile Thr Phe
 180 185 190
 Asn Arg Leu Tyr Pro Val Ile Leu Ile Ser Leu Thr Ile Phe Leu Asp
 195 200 205
 Ser Leu Ile Ile Leu Phe Ser Tyr Ile Leu Ile Leu Asn Thr Val Ile
 210 215 220
 Gly Ile Ala Ser Gly Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys Val
 225 230 235 240
 Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly Leu
 245 250 255
 Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His Ala
 260 265 270
 Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro Val
 275 280 285

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Ile Tyr Ser Ile Lys Thr Lys Gln Ile Gln Tyr Gly Ile Ile Arg Leu
 290 295 300

Leu Ser Lys His Arg Phe Ser Arg
 305 310

<210> 11
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 <212> PRT
 <213> CHICKEN

<400> 11
 Met Tyr Pro Arg Asn Ser Ser Gln Ala Gln Pro Phe Leu Leu Ala Gly
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Leu Pro Gly Met Ala Gln Phe His His Trp Val Phe Leu Pro Phe Gly
 20 25 30

Leu Met Tyr Leu Val Ala Val Leu Gly Asn Gly Thr Ile Leu Leu Val
 35 40 45

Val Arg Val His Arg Gln Leu His Gln Pro Met Tyr Tyr Phe Leu Leu
 50 55 60

Met Leu Ala Thr Thr Asp Leu Gly Leu Thr Leu Ser Thr Leu Pro Thr
 65 70 75 80

Val Leu Arg Val Phe Trp Leu Gly Ala Met Glu Ile Ser Phe Pro Ala
 85 90 95

Cys Leu Ile Gln Met Phe Cys Ile His Val Phe Ser Phe Met Glu Ser
 100 105 110

Ser Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Cys
 115 120 125

Pro Leu Arg Tyr Ser Ser Ile Leu Thr Gly Ala Arg Val Ala Gln Ile
 130 135 140

Gly Leu Gly Ile Ile Cys Arg Cys Thr Leu Ser Leu Leu Pro Leu Ile
 145 150 155 160

Cys Leu Leu Thr Trp Leu Pro Phe Cys Arg Ser His Val Leu Ser His
 165 170 175

Pro Tyr Cys Leu His Gln Asp Ile Ile Arg Leu Ala Cys Thr Asp Ala

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180 185 190
Thr Leu Asn Ser Leu Tyr Gly Leu Ile Leu Val Leu Val Ala Ile Leu
195 200 205
Asp Phe Val Leu Ile Ala Leu Ser Tyr Ile Met Ile Phe Arg Thr Val
210 215 220
Leu Gly Ile Thr Ser Lys Glu Glu Gln Thr Lys Ala Leu Asn Thr Cys
225 230 235 240
Val Ser His Phe Cys Ala Val Leu Ile Phe Tyr Ile Pro Leu Ala Gly
245 250 255
Leu Ser Ile Ile His Arg Tyr Gly Arg Asn Ala Pro Pro Ile Ser His
260 265 270
Ala Val Met Ala Asn Val Tyr Leu Phe Val Pro Pro Ile Leu Asn Pro
275 280 285
Val Leu Tyr Ser Met Lys Ser Lys Ala Ile Cys Lys Gly Leu Leu Arg
290 295 300
Leu Leu Cys Gln Arg Ala Ala Trp Pro Gly His Ala Gln Asn Cys
305 310 315
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Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
20 25 30
Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
35 40 45
Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
50 55 60
Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
65 70 75 80

Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
 85 90 95

Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
 100 105 110

Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
 115 120 125

Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly
 130 135 140

Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
 145 150 155 160

Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
 165 170 175

Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
 180 185 190

Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
 195 200 205

Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
 210 215 220

Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
 225 230 235 240

Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
 245 250 255

Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
 260 265 270

Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
 275 280 285

Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
 290 295 300

Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
 305 310 315 320

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 <213> MOUSE

<400> 13

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			20					25					30		
Thr	Trp	Leu	Ser	Ile	Pro	Phe	Cys	Leu	Met	Tyr	Ile	Ala	Ala	Val	Leu
		35					40						45		
Gly	Asn	Gly	Ala	Leu	Ile	Leu	Val	Val	Leu	Ser	Glu	Arg	Thr	Leu	His
	50					55					60				
Glu	Pro	Met	Tyr	Val	Phe	Leu	Ser	Met	Leu	Ala	Gly	Thr	Asp	Ile	Leu
65					70					75				80	
Leu	Ser	Thr	Thr	Thr	Val	Pro	Lys	Thr	Leu	Ala	Ile	Phe	Trp	Phe	His
				85					90					95	
Ala	Gly	Glu	Ile	Pro	Phe	Asp	Ala	Cys	Ile	Ala	Gln	Met	Phe	Phe	Ile
			100					105					110		
His	Val	Ala	Phe	Val	Ala	Glu	Ser	Gly	Ile	Leu	Leu	Ala	Met	Ala	Phe
		115						120					125		
Asp	Arg	Tyr	Val	Ala	Ile	Cys	Thr	Pro	Leu	Arg	Tyr	Ser	Ala	Val	Leu
		130					135					140			
Thr	Pro	Met	Ala	Ile	Gly	Lys	Met	Thr	Leu	Ala	Ile	Trp	Gly	Arg	Ser
145						150				155					160
Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ile	Phe	Leu	Leu	Lys	Arg	Leu	Ser	Tyr
			165						170					175	
Cys	Arg	Thr	Asn	Val	Ile	Pro	His	Ser	Tyr	Cys	Glu	His	Ile	Gly	Val
			180						185				190		
Ala	Arg	Leu	Ala	Cys	Ala	Asp	Ile	Thr	Val	Asn	Ile	Trp	Tyr	Gly	Phe
		195					200					205			
Ser	Val	Pro	Met	Ala	Ser	Val	Leu	Val	Asp	Val	Ala	Leu	Ile	Gly	Ile
		210					215					220			

Ser Tyr Thr Leu Ile Leu Gln Ala Val Phe Arg Leu Pro Ser Gln Asp
225 230 235 240

Ala Arg His Lys Ala Leu Asn Thr Cys Gly Ser His Ile Gly Val Ile
245 250 255

Leu Leu Phe Phe Ile Pro Ser Phe Phe Thr Phe Leu Thr His Arg Phe
260 265 270

Gly Lys Asn Ile Pro His His Val His Ile Leu Leu Ala Asn Leu Tyr
275 280 285

Val Leu Val Pro Pro Met Leu Asn Pro Ile Ile Tyr Gly Ala Lys Thr
290 295 300

Lys Gln Ile Arg Asp Ser Met Thr Arg Met Leu Ser Val Val Trp Lys
305 310 315 320

Ser

<210> 14

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<212> PRT

<213> MOUSE

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Met Lys Val Ala Ser Ser Phe His Asn Asp Thr Asn Pro Gln Asp Val
1 5 10 15

Trp Tyr Val Leu Ile Gly Ile Pro Gly Leu Glu Asp Leu His Ser Trp
20 25 30

Ile Ala Ile Pro Ile Cys Ser Met Tyr Ile Val Ala Val Ile Gly Asn
35 40 45

Val Leu Leu Ile Phe Leu Ile Val Thr Glu Arg Ser Leu His Glu Pro
50 55 60

Met Tyr Phe Phe Leu Ser Met Leu Ala Leu Ala Asp Leu Leu Leu Ser
65 70 75 80

Thr Ala Thr Ala Pro Lys Met Leu Ala Ile Phe Trp Phe His Ser Arg
85 90 95

Gly Ile Ser Phe Gly Ser Cys Val Ser Gln Met Phe Phe Ile His Phe

0906459.09260

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100	105	110
Ile Phe Val Ala Glu Ser Ala	Ile Leu Leu Ala Met	Ala Phe Asp Arg
115	120	125
Tyr Val Ala Ile Cys Tyr Pro	Leu Arg Tyr Thr Thr	Ile Leu Thr Ser
130	135	140
Ser Val Ile Gly Lys Ile Gly Thr	Ala Ala Val Val Arg Ser Phe	Leu
145	150	155 160
Ile Cys Phe Pro Phe Ile Phe	Leu Val Tyr Arg Leu Leu Tyr	Cys Gly
165	170	175
Lys His Ile Ile Pro His Ser Tyr	Cys Glu His Met Gly Ile Ala	Arg
180	185	190
Leu Ala Cys Asp Asn Ile Thr Val	Asn Ile Ile Tyr Gly Leu Thr	Met
195	200	205
Ala Leu Leu Ser Thr Gly Leu Asp	Ile Leu Leu Ile Ile Ile Ser	Tyr
210	215	220
Thr Met Ile Leu Arg Thr Val Phe	Gln Ile Pro Ser Trp Ala Ala	Arg
225	230	235 240
Tyr Lys Ala Leu Asn Thr Cys Gly	Ser His Ile Cys Val Ile Leu	Leu
245	250	255
Phe Tyr Thr Pro Ala Phe Phe Ser	Phe Phe Ala His Arg Phe Gly	Gly
260	265	270
Lys Thr Val Pro Arg His Ile His	Ile Leu Val Ala Asn Leu Tyr	Val
275	280	285
Val Val Pro Pro Met Leu Asn Pro	Ile Ile Tyr Gly Val Lys Thr	Lys
290	295	300
Gln Ile Gln Asp Arg Val Val Phe	Leu Phe Ser Ser Val Ser Thr	Cys
305	310	315 320
Gln His Asp Ser Arg Cys		
325		

<210> 15
<211> 318
<212> PRT

<213> MOUSE

<400> 15

Met Ser Pro Gly Asn Ser Ser Trp Ile His Pro Ser Ser Phe Leu Leu
1 5 10 15

Leu Gly Ile Pro Gly Leu Glu Glu Leu Gln Phe Trp Leu Gly Leu Pro
20 25 30

Phe Gly Thr Val Tyr Leu Ile Ala Val Leu Gly Asn Val Ile Ile Leu
35 40 45

Phe Val Ile Tyr Leu Glu His Ser Leu His Gln Pro Met Phe Tyr Leu
50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Leu Gly Leu Ser Thr Ala Thr Val
65 70 75 80

Pro Arg Ala Leu Gly Ile Phe Trp Phe Gly Phe His Lys Ile Ala Phe
85 90 95

Arg Asp Cys Val Ala Gln Met Phe Phe Ile His Leu Phe Thr Gly Ile
100 105 110

Glu Thr Phe Met Leu Val Ala Met Ala Phe Asp Arg Tyr Ile Ala Ile
115 120 125

Cys Asn Pro Leu Arg Tyr Asn Thr Ile Leu Thr Asn Arg Thr Ile Cys
130 135 140

Ile Ile Val Gly Val Gly Leu Phe Lys Asn Phe Ile Leu Val Phe Pro
145 150 155 160

Leu Ile Phe Leu Ile Leu Arg Leu Ser Phe Cys Gly His Asn Ile Ile
165 170 175

Pro His Thr Tyr Cys Glu His Met Gly Ile Ala Arg Leu Ala Cys Val
180 185 190

Ser Ile Lys Val Asn Val Leu Phe Gly Leu Ile Leu Ile Ser Met Ile
195 200 205

Leu Leu Asp Val Val Leu Ser Ala Leu Ser Tyr Ala Lys Ile Leu His
210 215 220

Ala Val Phe Lys Leu Pro Ser Trp Glu Ala Arg Leu Lys Ala Leu Asn
225 230 235 240

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Thr Cys Gly Ser His Val Cys Val Ile Leu Ala Phe Phe Thr Pro Ala
 245 250 255

Phe Phe Ser Phe Leu Thr His Arg Phe Gly His Asn Ile Pro Arg Tyr
 260 265 270

Ile His Ile Leu Leu Ala Asn Leu Tyr Val Ile Ile Pro Xaa Ala Leu
 275 280 285

Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys Gln Ile Gln Asp Arg Ala
 290 295 300

Val Thr Ile Leu Cys Asn Glu Val Gly Gln Leu Ala Asp Asp
 305 310 315

<210> 16
 <211> 316
 <212> PRT
 <213> MOUSE

<400> 16
 Met Ile Lys Phe Asn Gly Ser Val Phe Met Pro Ser Val Leu Thr Leu
 1 5 10 15

Val Gly Ile Pro Gly Leu Glu Ser Val Gln Cys Trp Ile Gly Ile Pro
 20 25 30

Phe Cys Val Met Tyr Ile Ile Ala Met Ile Gly Asn Ser Leu Ile Leu
 35 40 45

Val Ile Ile Lys Ser Glu Lys Ser Leu His Ile Pro Met Tyr Ile Phe
 50 55 60

Leu Ala Ile Leu Ala Val Thr Asp Ile Ala Leu Ser Thr Cys Ile Leu
 65 70 75 80

Pro Lys Met Leu Gly Ile Phe Trp Phe His Met Pro Gln Ile Ser Phe
 85 90 95

Asp Ala Cys Leu Leu Gln Met Glu Leu Ile His Ser Phe Gln Ala Thr
 100 105 110

Glu Ser Gly Ile Leu Leu Ala Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125

Cys Asn Pro Leu Arg His Ala Thr Ile Phe Ser Pro Gln Leu Thr Thr
 130 135 140

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Cys Leu Gly Ala Gly Ala Leu Leu Arg Ser Leu Ile Thr Thr Phe Pro
145 150 155 160

Leu Ile Leu Leu Ile Lys Phe Cys Leu Lys Tyr Phe Arg Thr Thr Ile
165 170 175

Ile Ser His Ser Tyr Cys Glu His Met Ala Ile Val Lys Leu Ala Ala
180 185 190

Gln Asp Ile Arg Ile Asn Lys Ile Cys Gly Leu Leu Val Ala Phe Ala
195 200 205

Ile Leu Gly Phe Asp Ile Val Phe Ile Thr Phe Ser Tyr Val Arg Ile
210 215 220

Phe Ile Thr Val Phe Gln Leu Pro Gln Lys Glu Ala Arg Phe Lys Ala
225 230 235 240

Phe Asn Thr Cys Ile Ala His Ile Cys Val Phe Leu Gln Phe Tyr Leu
245 250 255

Leu Ala Phe Phe Ser Phe Phe Thr His Arg Phe Gly Ala His Ile Pro
260 265 270

Pro Tyr Val His Ile Leu Leu Ser Asp Leu Tyr Leu Leu Val Pro Pro
275 280 285

Phe Leu Asn Pro Ile Val Tyr Gly Ile Lys Thr Lys Gln Ile Arg Asp
290 295 300

Gln Val Leu Lys Met Phe Phe Ser Lys Lys Pro Leu
305 310 315

<210> 17

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 17

Met Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10 15

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln
20 25

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 18
Arg Thr Glu His Ser Leu His Glu Pro Met Tyr
1 5 10

<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 19
Asn Ser Thr Thr Ile Gln Phe Asp Ala Cys Leu Leu Gln Met
1 5 10

<210> 20
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthesized
peptide

<400> 20
His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr Lys
1 5 10 15

<210> 21
<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 21

Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu Ser His Ser Tyr Cys
1 5 10 15

Leu His Gln Asp Val Met Lys Leu Ala Cys Asp Asp Ile Arg
20 25 30

<210> 22

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 22

Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala
1 5 10

<210> 23

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 23

His Arg Phe Ser Lys Arg Arg Asp Ser Pro
1 5 10

<210> 24

<211> 22

<212> PRT

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: Synthesized
peptide

<400> 24

Lys Thr Lys Glu Ile Arg Gln Arg Ile Leu Arg Leu Phe His Val Ala
1 5 10 15

Thr His Ala Ser Glu Pro
20

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Forward GPCR9
primer-

<400> 25

cctgtgctca acccaattgt ct

22

<210> 26

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reverse GPCR9
primer-

<400> 26

actgacacct agggctctga ag

22

<210> 27

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-F3
forward primer

<400> 27

agccgagcca catcgct

17

<210> 28

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-R1
reverse primer

<400> 28

gtgaccaggc gcccaatac

19

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: GAPDH-PVIC
Taqman(R) Probe

<400> 29

caaatccgtt gactccgacc ttcacctt

28

<210> 30

<211> 39

<212> DNA

<213> Artificial Sequence

<400> 30

cccaagcttg caccatgatg gtggatccca atggcattg

39

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 3'
primer

<400> 31

gaagatctct agggctctga agcgtgtgtg gcc

33

<210> 32

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: HGPRBMY4 3'
primer- Flag tag

<400> 32

gaagatctct acttgctgctc gtcgtccttg tagtccatgg gctctgaagc gtgtgtggc 59

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 33

Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu
1 5 10

<210> 34

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 34

Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
1 5 10

<210> 35

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 35

Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr
1 5 10

<210> 36

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 36

Ala Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu
1 5 10

<210> 37

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 37

His Arg Phe Ser Lys Arg Arg Asp Ser Pro Leu Pro Val Ile
1 5 10

<210> 38

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 38

T09260" 65499660

Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 39
Ile Ala Val Leu Gly Asn Leu Thr Ile Ile Tyr Ile Val Arg
1 5 10

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 40
Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe Asp Ala
1 5 10

<210> 41
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 41
Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
1 5 10 15

<210> 42
<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 42

Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe
1 5 10 15

<210> 43

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 43

Ile His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala
1 5 10 15

<210> 44

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 44

Gln Ala Lys Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe
1 5 10 15

<210> 45

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 45

His Ser Leu Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe
1 5 10 15

Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
20 25

<210> 46

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 1;

N=A+G+C+T; K=C+G+T

<400> 46

cgaagcgtaa gggcccagcc ggccnnknnk nnknnknnkn nknnknnknn knnknnknnk 60
nnknnknnkn nknnknnknn knnkccgggt ccgggcggc 99

<210> 47

<211> 95

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligo 2;

N+A+G+C+T; V=C+A+G

<400> 47

aaaaggaaaa aagcggccgc vnnvnnvnnv nnvnnvnnvn nvnnvnnvnn vnnvnnvnnv 60
nnvnnvnnvn nvnnvnnvnn gccgcccgga cccgg 95

<210> 48

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 48

Pro Gly Pro Gly Gly

0906459 092601
T09260" 6549660

1

5

<210> 49

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 49

gcagcagcgg ccgccagttc tggttggcct tcccattg

38

<210> 50

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 50

gcagcagtcg acgggctctg aagcgtgtgt ggccac

36

<210> 51

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic 5'
Primer

<400> 51

gcagcagcgg ccgcatgatg gtggatccca atggcaatg

39

<210> 52

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

T09260"6549660

<223> Description of Artificial Sequence: Synthetic 3'
Primer

<400> 52

gcagcagtcg accttcactc catagacaat tggggttg

37

<210> 53

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 53

Gly Asp Phe Trp Tyr Glu Ala Cys Glu Ser Ser Cys Ala Phe Trp
1 5 10 15

<210> 54

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 54

Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
1 5 10 15

<210> 55

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55

Phe Ala Gly Gln Ile Ile Trp Tyr Asp Ala Leu Asp Thr Leu Met
1 5 10 15

<210> 56
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 56
Leu Ile Phe Phe Asp Ala Arg Asp Cys Cys Phe Asn Glu Gln Leu
1 5 10 15

<210> 57
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57
Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
1 5 10 15

<210> 58
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 58
Arg Ile Val Pro Asn Gly Tyr Phe Asn Val His Gly Arg Ser Leu
1 5 10 15

<210> 59
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 59

Trp Glu Arg Ser Ser Ala Gly Cys Ala Asp Gln Gln Tyr Arg Cys
1 5 10 15

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 60

Tyr Phe Ser Asp Gly Glu Ser Phe Phe Glu Pro Gly Asp Cys Cys
1 5 10 15

09060459 09260 65499660